

Shown is the 3'UTR of the human IL1B sequence from accession number M15330.

* Represents the stop codon.

*AGAGAGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCCTAG
GGCTGGCAGAAAGGAACAGAAAGGTTTGTGAGTACGGCTATAGCCTGGAC
TTTCCTGTGTCTACACCAATGCCCCAACTGCCCTGCTTAGGGTAGTGCTAA
GAGGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCC
AATCCCAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTCCTACTCACT
TAAAGCCCGCTGACAGAAACACGGCCACATTTGGTTCTAAGAAACCCCTC
TGTCATTTCGCTCCCACATTCTGATGAGCAACCGCTTCCCTATTTATTTATT
TATTTGTTGTTTTATTTCATTGGTCTAATTTATTCAAAGGGGCAAG
AAGTAGCAGTGTCTGTAAAGAGCCCTAGTTTTTAATAGCTATGGAATCAAT
TCAATTGGACTGGTGTCTCTCTTTAAATCAAGTCCTTAAATTAAGACTG
AAAATATATAAGCTCAGATTTTTAAATGGGAATTTTATATAAATGAGCAAA
TATCATACTGTTCAATGGTTCTGAAATAAACTTCTCTGAAG

FIGURE 1

ATGGCTTCCCT**ATTATTTATTATT**TGTTGTCCAACCT
|||||
GGATACCGAAGGAT**AAATAAATAA**AAACAACAGGTT

FIGURE 2

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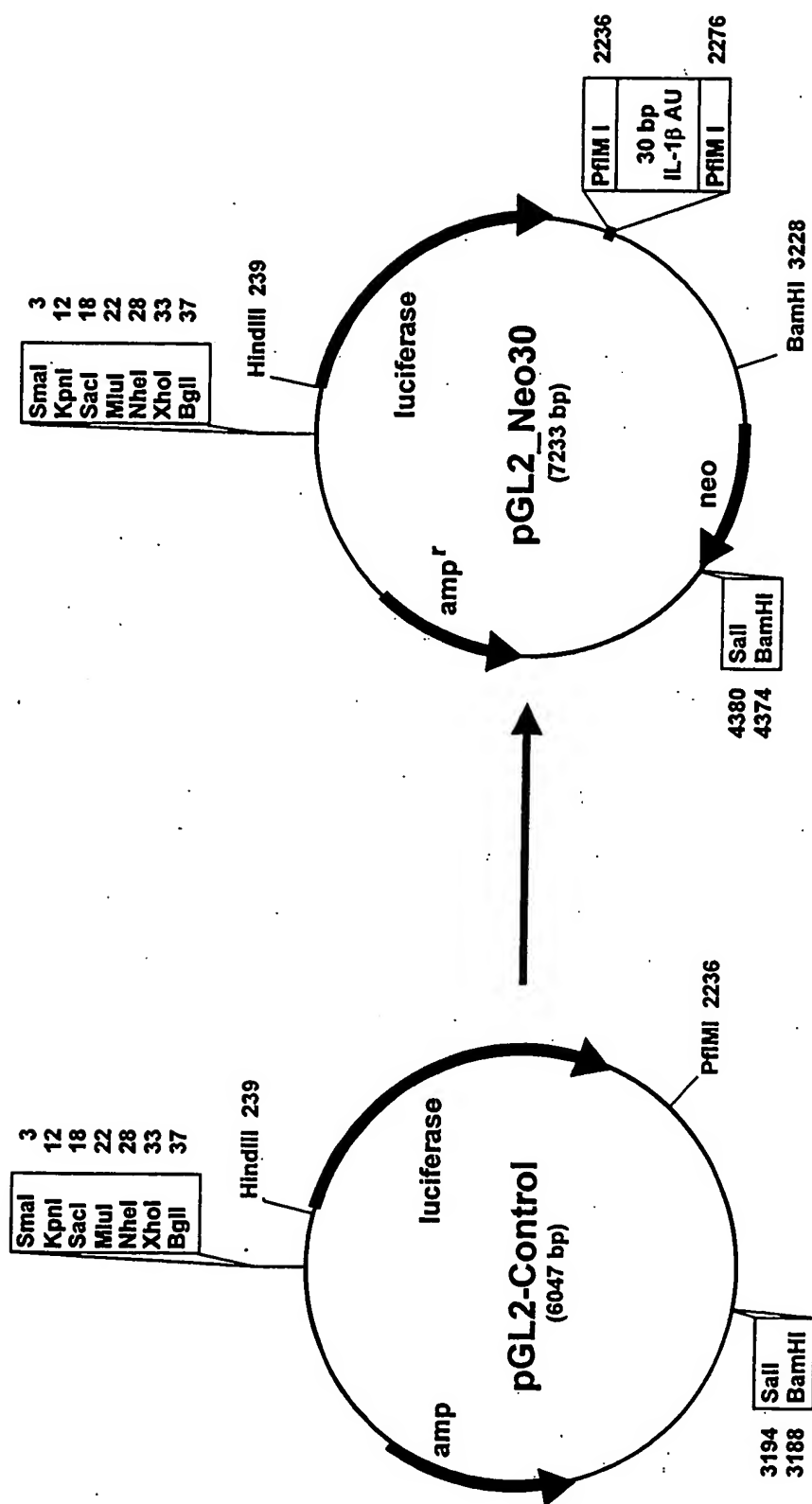


FIGURE 3 A

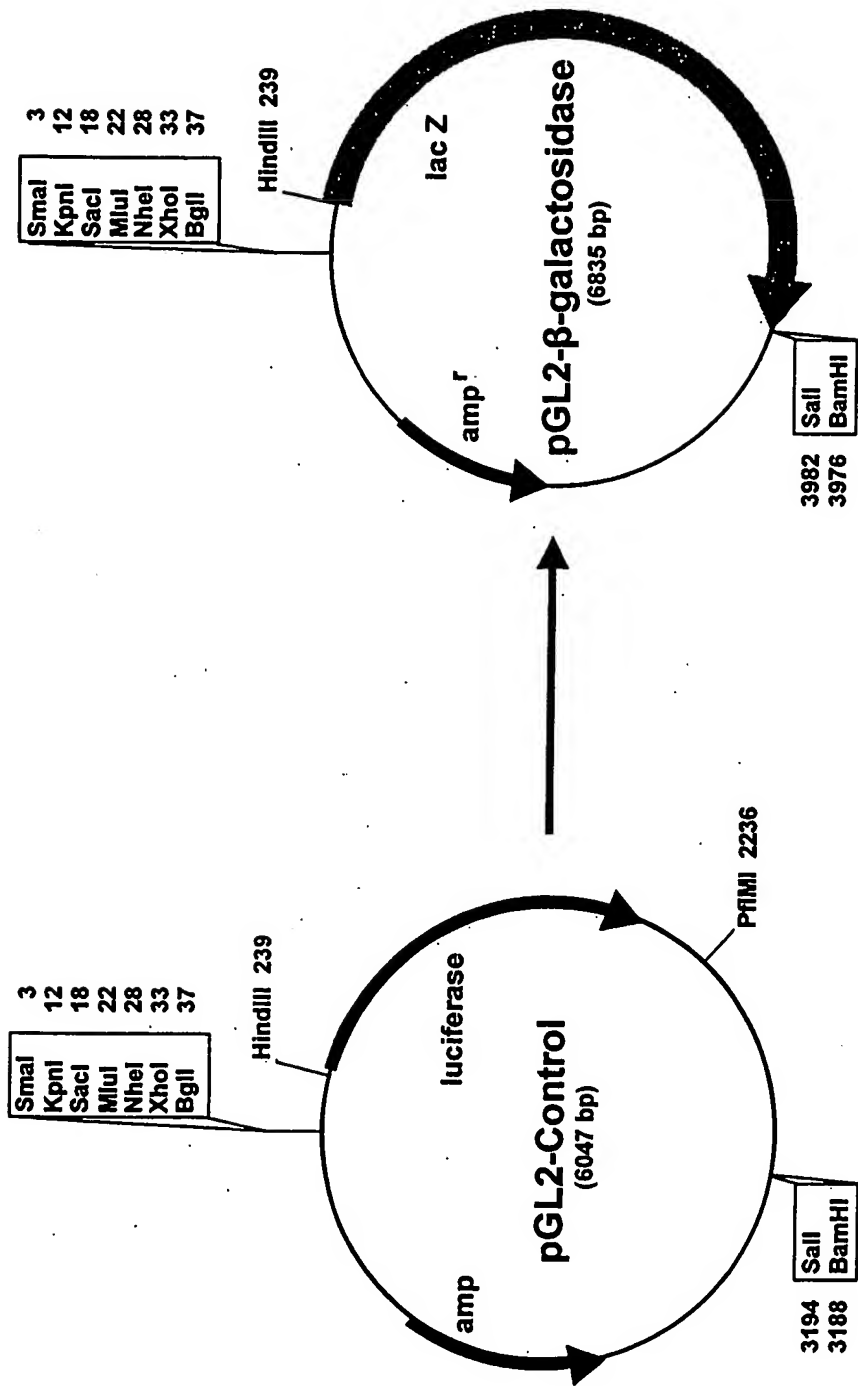


FIGURE 3 B

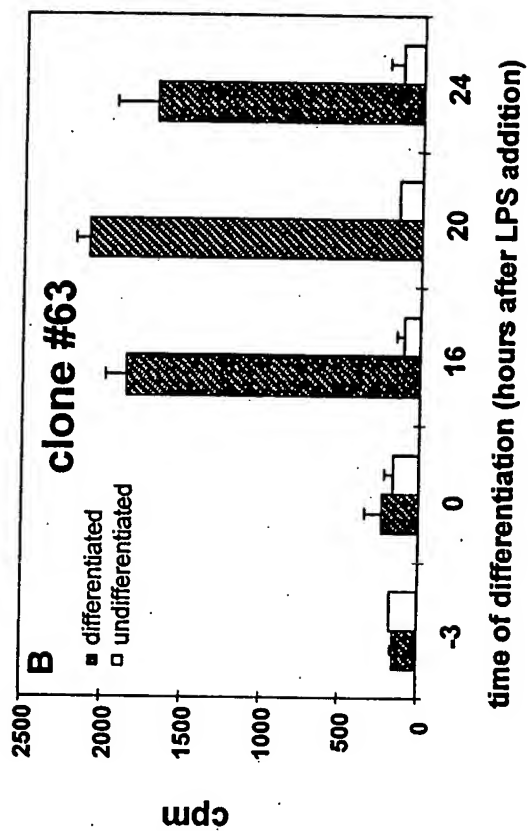
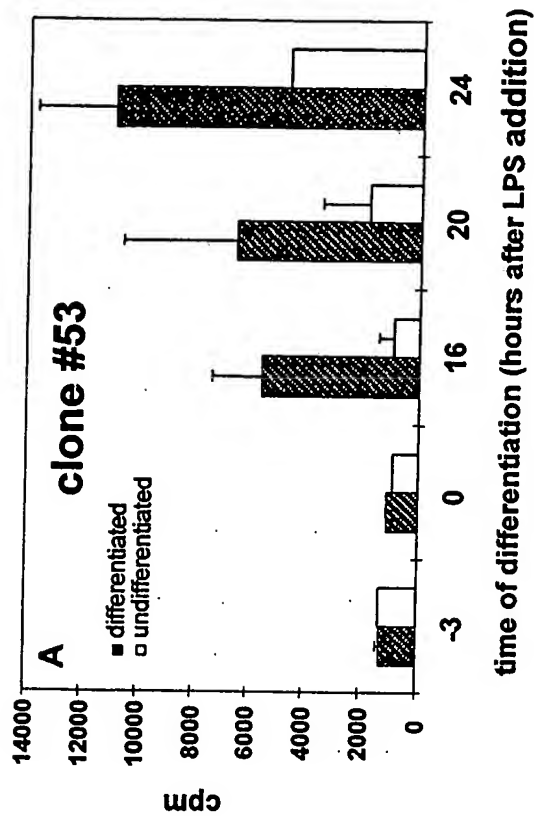


FIGURE 4

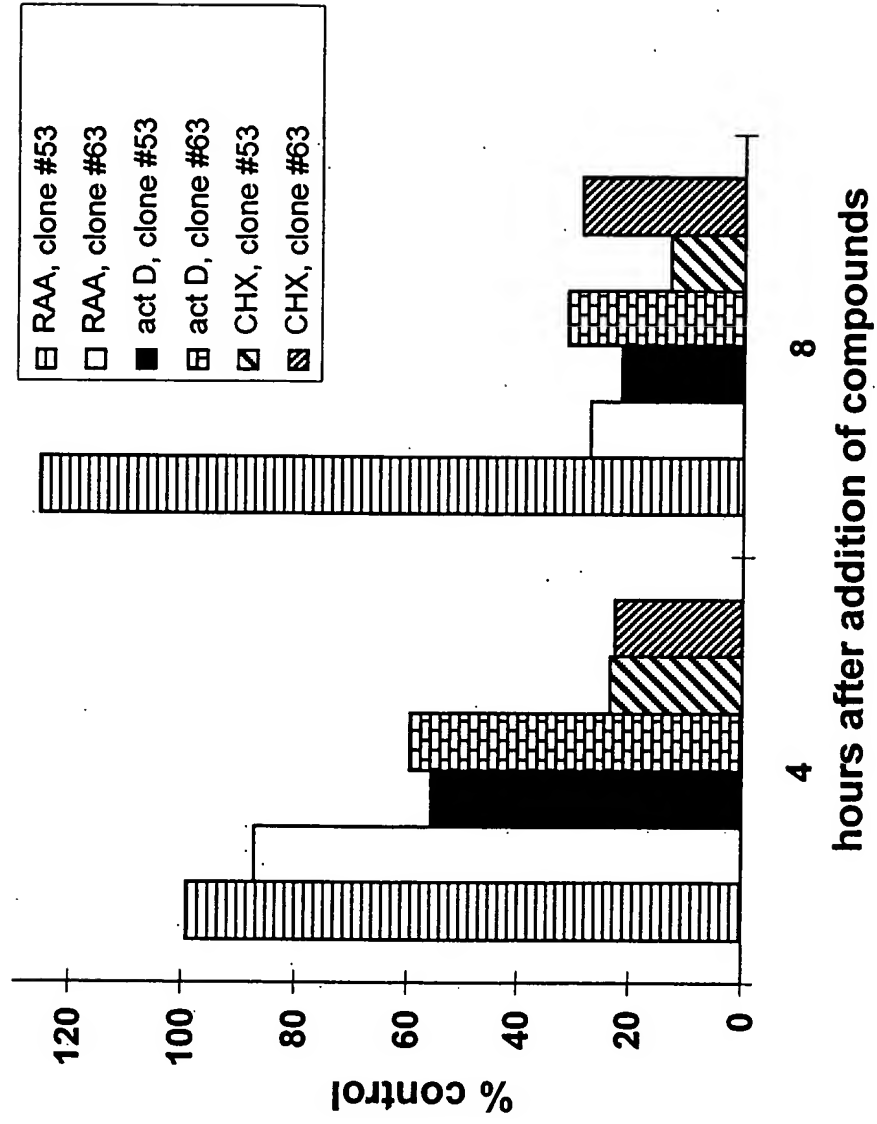


FIGURE 5

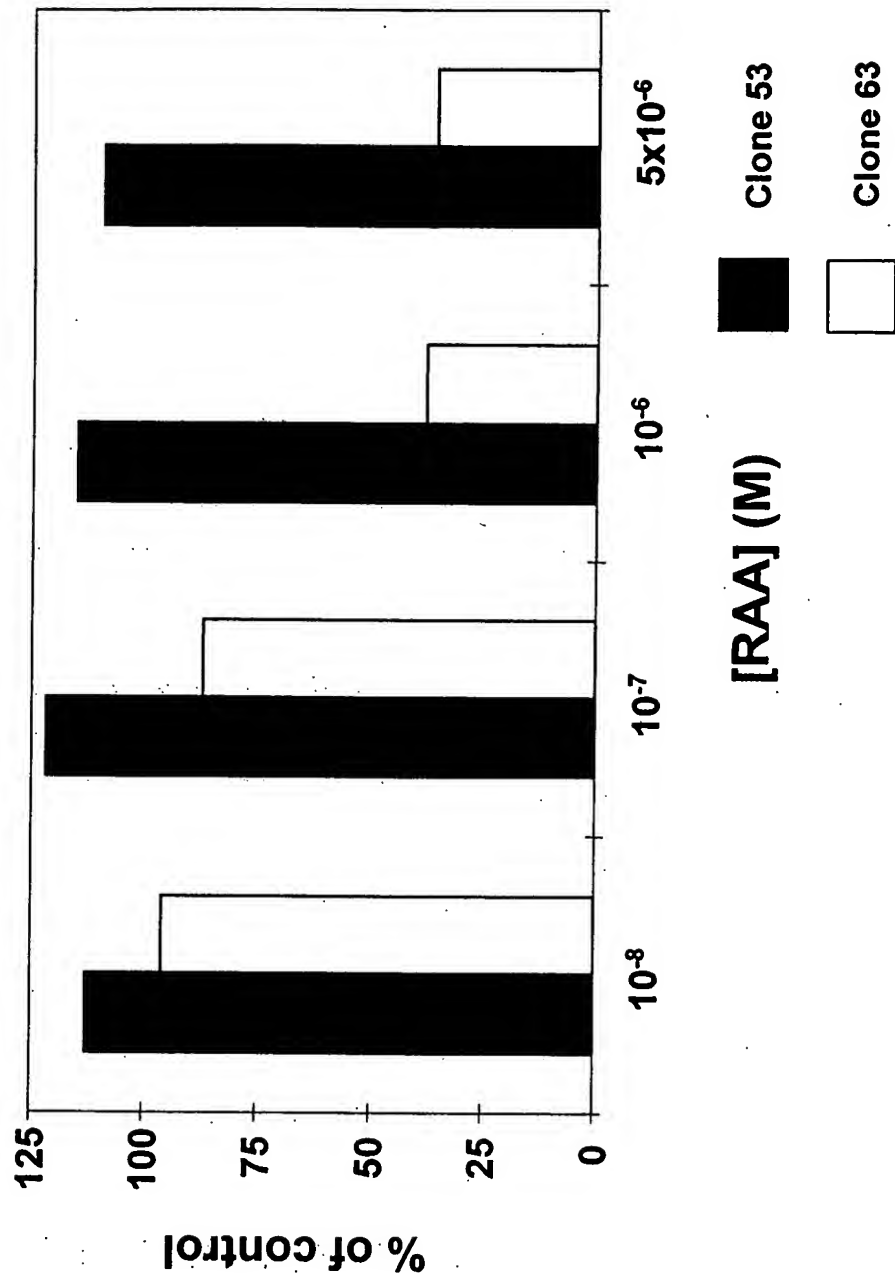


FIGURE 6

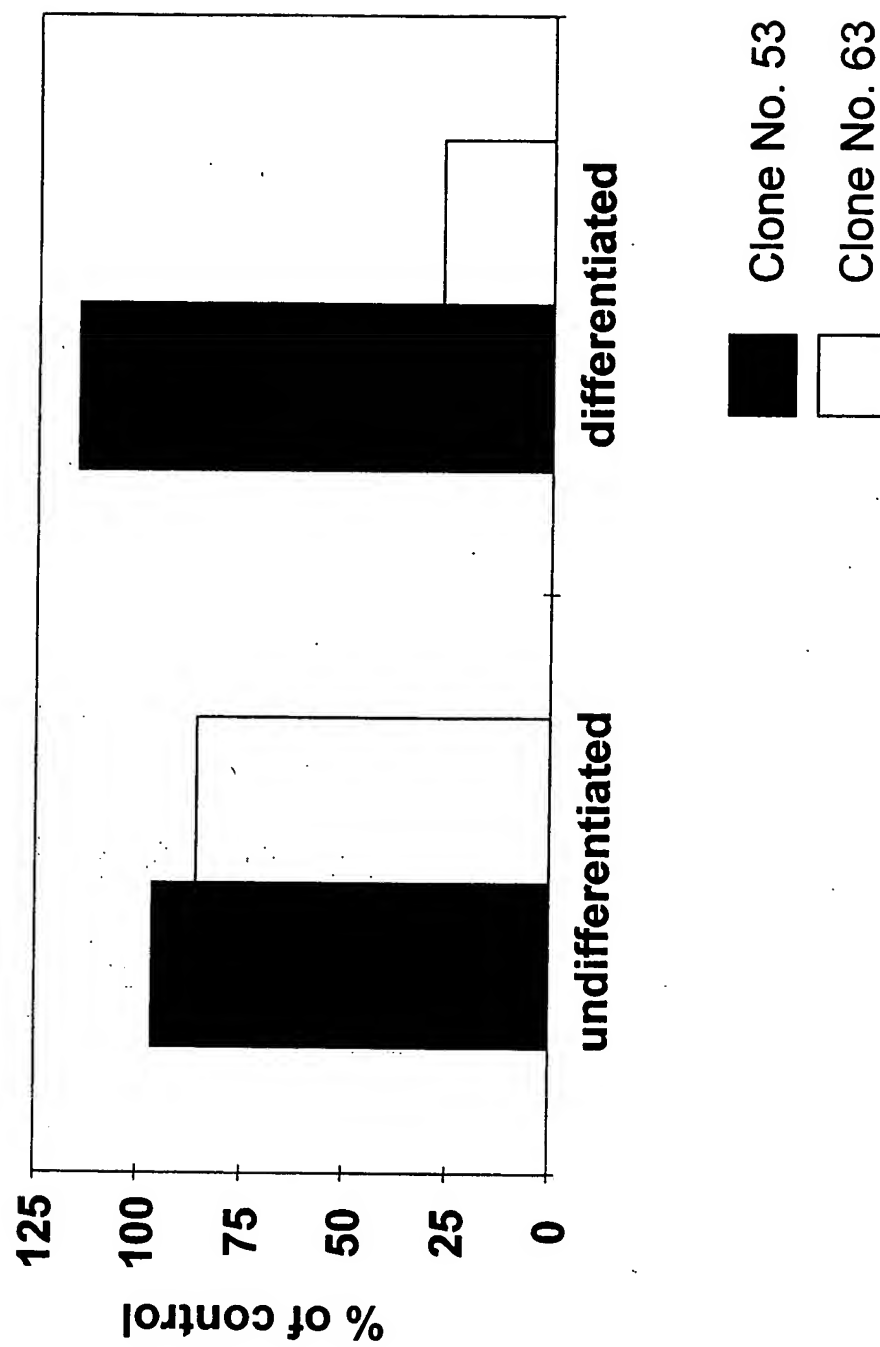


FIGURE 7

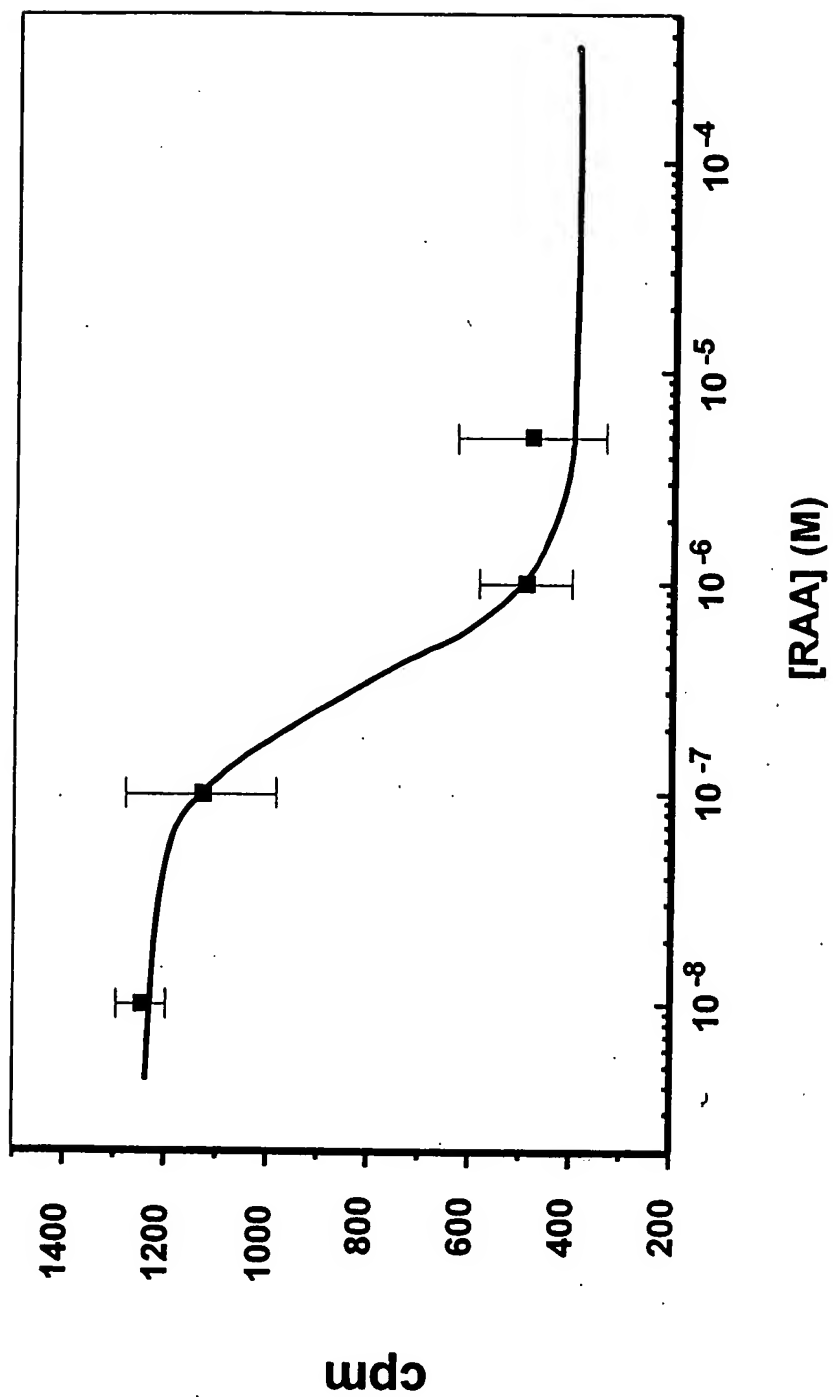


FIGURE 8

APP construct: 

■ AUUUA {Bold/Underline}
★ potential polyA signal sequence {Bold/Italics}
Restriction Sites {Bold}

NotI

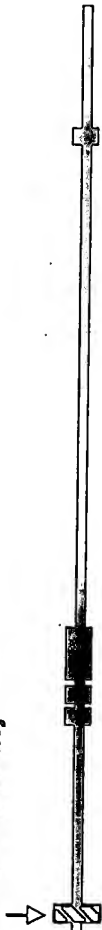
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1  GCGGCGGCCA CAGCAGCCTC TGAAGTTGGA CAGCAAAACC ATTGCTTCAC TACCCATCGG TGTCATTTA TAGAATAATG TGGGAAGAAA CAAACCCGTT
101 TTATGATTTA CTCAATTATG CCTTTTGACA GCTGTGCTGT AACACAAGTA GATGCCTGAA CTTGAAATTA TCCACACATC AGTAATGTAT TCTATCTCTC
201 TTTACATTTT GGTCTCTATA CTACATTATT AATGGGTTTT GTGTACTGTA AAGAATTAG CTTGATCATA CTAGTGCATG AATAGATTCT CTCCTGATTA
301 TTATACACAT AGCCCTTAG CCAGTTGTAT ATTATTCTTG TGGTTTGA CCAATTAAG TCCTACTTTA CATATGCTTT AGAATCGAT GGGGGATGCT
401 TCATGTGAAC GTGGGAGTTC AGCTGCTTCT CTTCCTTTC CTGATCACTA TGCATTTTAA AGTTAAACAT TTTTAAGTAT TTCAGATGCT
501 TTAGAGAGAT TTTTTTTTCC ATGACTGCAAT TTACTGTAC AGATTGCTGC TTCGCTATA TTGTGATAT AGGAATTAAG AGGATACACA CGTTTGTTC
601 TTCGTGCCCTG TTTTATGTGC ACACATTAGG CATTGAGACT TCAAGCTTTT CTTTTTTTGT CCACGTATCT TTGGGTCTTT GATAAAGAAA AGAATCCCTG
701 TTCATTGTAA GCACTTTAC GGGGCGGGTG GGGAGGGGTG CTCTGCTGGT CTTCAATTAC CAAGAATTCT CCAAAACAAT TTCTGCAGG ATGATTGTAC
801 AGAATCATTG CTTATGACAT GATCGCTTTC TACACTGTAT TACATAAATA AATTAAATAA AATAACCCCG GCCAAGACTT TTCCTTTGAAG GATGACTACA
901 GACATTAAAT AATCGAAGTA ATTTTGGGTG GGGAGAGAG GCAGATTCAA TTTTCTTTAA CCAGTCTGAA GTTTCATTTA TGATACAAAA GAAGATGAAA
1001 ATGGAAGTGG CAATATAAGG GGATGAGGAA GGCATGCCCTG GACAACCCT TCCTTTAAGA TGTGCTTCA ATTTGTATAA AATGGTGTTC TCATGTAGCG
1101 GCGGC
NotI
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FIGURE 9

Length: 1105 bp

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stop codon {***Bold/Italics/Underline***}



bcl-2α-joint construct:

□ AUUUA {**Bold/Underline**}
Restriction Sites {**Bold**}

Not

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1  GCGSCGCTG AAGTCAACAT GCCTGCCCA. AACAAATATG CAAAGGTTT ACTAAGCAG TAGAATAAT ATGATTGTC AGTGATGAC CATGAACAA
101 AGCTGCAGGC TGTTTAAGAA AAAATAACAC ACATATAAAC ATCACACACA CAGACAGACA CAACAATTAA CAGTCTTCAG GCAAAACGTC
201 GAATCAGCTA TTTACTGCCA AAGGGAATA. TCATTTATTT TTTACATTAT TAAGAAAAAA AGATTATTT ATTTAAGACA GTCCCATCAA AACTCCTGTC
301 TTTGGAAATC CGACCACTAA TTGCCAAGCA CCGCTTCGTG TGGCTCCACC TGGATGTTCT GTGCCTGTAA ACATAGATTG GCTTTCCATG TTGTTGGCCG
401 GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGG AAGCTGGCTT TCTGGCTGCT GGAGGCTGGG GAGAAGGTGT TCATTCACCT
501 GAATTTCTTT GCCCTGGGG CTGTGATATT AACAGAGGGA GGGTTCCTGT GGGGGGAAGT CCATGCCCTCC CTGGCCTGAA GAAGAGACTC TTTGCATATG
601 ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT GGACCTAGTA CCCACTGAGA TTTCCACGCC GAAGGACAGC GATGGGAAAA
701 ATGCCCTTAA ATCATAGGAA AGTATTTTTT TAAGCTACCA ATTGTGCCGA GAAAAGCATT TTAGCAATTT ATACAATATC ATCCAGTACC TTAAGCCCTG
801 ATTGTGTATA TTCATATATT TTGGATACGC ACCCCCCAAC TCCCAATACT GGCTCTGTCT GAGTAAGAAA CAGATCCTC TGGAACTTGA GGAAGTGGGG
901 CCGC

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Not

Length: 904 bp

FIGURE 10

stop codon {**Bold/Italics/Underline**}



■ AUUUA {**Bold/Underline**}
Restriction Sites {**Bold**}

NotI

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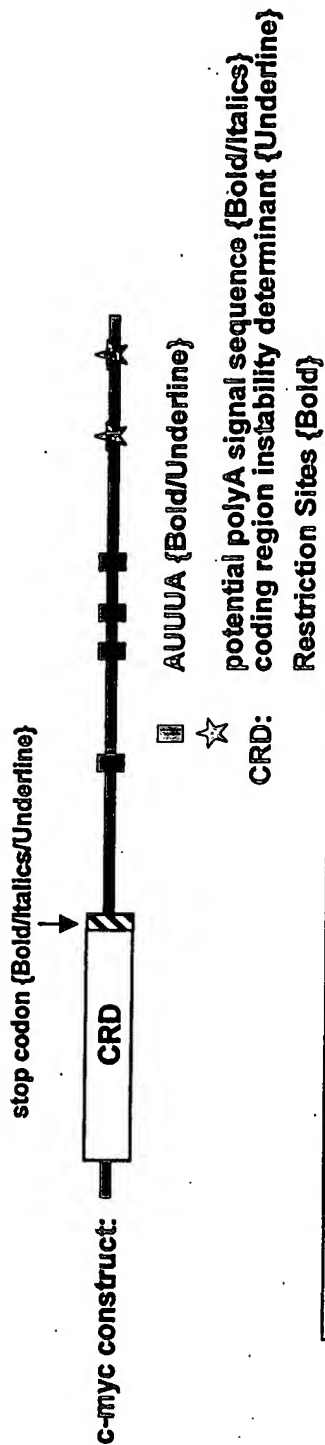
1  GCGGGCGCTG AAGTCAACAT GCCTGCCCA AACAAATATG CAAAAGGTTT
51  ACTAAGCAG TAGAATAAT ATGCATTGTC AGTGATGTAC CATGAACAA
101 AGCTGCAGGC TGTTTAAGAA AAAATAACAC ACATATAAAC ATCACACACA
151 CAGACAGACA CACACACACA CAACAATTAA CAGTCTTCAG GCAAAACGTC
201 GAATCAGCTA TTTACTGCCA AAGGGAATA TCATTTATTT TTTACATTAT
251 TAAGAAAAAA AGATTATTTT ATTTAAGACA GTCCCATCAA AACTCTGTGTC
301 TTTGGAATC CGACCACTAA TTGCCAAGCA CCGCTTCCTG TGGCTCCACC
351 TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCANG TTGTTGGCCG
401 GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTTGGG
451 AAGCTGGCTT TCTGGCTGCT GGAGGCTGGG GAGAAGTGT TCATTCACTT
501 GCATTTCITT GCCCTGGGG CTGTGATATT AACAGAGGGA GGGTCCCTGT
551 GGGGGGAAGT CCATGCCTCC CTGGCCTGAA GAAGAGACTC TTTGCATATG
601 ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT
651 GGACCTAGTA CCCACTGAGA TTTCCACGCC GAAGGACAGC GATCGGAAAA
701 ATCGGGCCGC

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NotI

Length: 710 bp

FIGURE 11



| | | | | | |
|-----|------------|------------|------------|-------------|-------------|
| 1 | CGCGCGCTC | GGAGCTTTTT | TGCCCTGCCG | GACCAGATCC | CGGAGTTGGA |
| 51 | AAACAATGAA | AAGGCCCCCA | AGGTAGTTAT | CCTTAAAAAA | GCCACAGCAT |
| 101 | ACATCCTGTC | CGTCCAAGCA | GAGGAGCAAA | AGCTCAITTC | TGAAGAGGAC |
| 151 | TTGTTGCGGA | AACGACGAGA | ACAGTTGAAA | CACAAACTTG | AACAGCTACG |
| 201 | GAACTCTTGT | GCGTAAGGAA | AAGTAAGGAA | AACGATTCCCT | TCTGACAGAA |
| 251 | ATGTCCTGAG | CAATCACCTA | TGAACCTTGT | TCAAATGCAT | GATCAAAATGC |
| 301 | AACCTCACAA | CCTTGGCTGA | GTCTTGAGAC | TGAAAGATTT | AGCCATAATG |
| 351 | TAAACTGCCT | CAAATTGGAC | TTTGGGCATA | AAAGAACTTT | TTTATGCTTA |
| 401 | CCATCTTTTT | TTTTTCTTTA | ACAGATTTGT | ATTTAAGAAT | TGTTTTTAAA |
| 451 | AAATTTTAAG | ATTACACAA | TGTTTCTCTG | TAAATATTGC | CATTAAATGT |
| 501 | AAATAACTTT | AATAAAACGT | TTATAGCAGT | TACACAGAAT | TTCAATCCTA |
| 551 | GTATATAGTA | CCTAGTATTA | TAGGTACTAT | AAACCCTAAT | TTTTTTTATT |
| 601 | TAAGTACATT | TGCTTTTTTA | AAGTTGATTT | TTTCTATTG | TTTTTAGAAA |
| 651 | AAATAAATA | ACTGGCAAT | ATATCAITGA | GCCATATG | |

Length: 688 bp

FIGURE 12

stop codon (***UAA***)

TNF- α construct:



■ AUUUA (***UAA***)

☆ Potential polyA signal sequence (***UAA***)

Restriction Sites (***UAA***)

| | | | | | | |
|-----|-----------|------------|------------|-----------|-----------|------------|
| 1 | CGGCGGCTG | AGGAGGACGA | ACATCCAACC | TTCCCAACG | CCTCCCTGC | CCCAATCCCT |
| 61 | TTATTACCC | CTCCTTCAG | CACCCCTCA | CTCTTCTGG | TCAAAAGAG | AATTGGGGG |
| 121 | TTAGGGTCG | AACCCAAAG | CTAGACTTT | AGCAACAAG | CCACCACTT | GAACCTGGG |
| 181 | ATTAGGAAT | GTGTGGCTG | CACAGTGA | TGCTGGCA | CACTAAGA | TCAAACTGG |
| 241 | GCCTCCAG | CTCACTGGG | CCTACAGCT | TGATCCCTG | CATCTGGA | CTGGAGACCA |
| 301 | GGGAGCCTT | GGTCTGGCC | AGAATGCTG | AGGACTTG | AGACCTCA | CTAGAAATTG |
| 361 | ACACAAGTG | ACCTTAGGC | TTCTCTCTC | CAGATGTTT | CAGACTTC | TGAGACACGG |
| 421 | AGCCAGCCC | TCCCCATGG | GCCAGCTCC | TCTATTATG | TTTGACTTG | TGATTATTGA |
| 481 | TTATTATT | ATTATTATT | TATTACAGA | TGAATGATT | TATTGGGAG | ACCGGGGTAT |
| 541 | CCTGGGGG | CCAATGTAG | AGTGCCTTG | GCTCAGAC | ATTTCCGTG | AAAACGGAGC |
| 601 | TGAACAAT | AGTGTCCCA | TGTAGCCCC | TGGCCTCTG | GCCTCTTTT | GATTATGTTT |
| 661 | TTAAATAT | TATCTGATT | AAGTTGTCT | AACATGCTG | ATTTGGTGC | CAACTGTCAC |
| 721 | TCATTGCT | GCCCTGCTC | CCCAGGGAG | TTGTGCTGT | AATGCCCTA | CTATTCAGTG |
| 781 | GCGAGAAAT | AAGTTTGCT | CATATG | | | |

NdeI

Length: 806 bp

FIGURE 13

stop codon {***Bold/Italics/Underline***}

IL-1 β construct:



■ AUUUA {***Bold/Underline***}

☆ Potential polyA signal sequence {***Bold/Italics***}

Restriction Sites {***Bold***}

| No | Seq |
|-----|--|
| 1 | CGGCGCGCTA <u>AAGAGAGCTG</u> TACCCAGAGA GTCCTGTGCT GAATGTGGAC |
| 51 | TCAATCCCTA GGGCTGGCAG AAAGGGAACA GAAAGTTTT TGAGTACGGC |
| 101 | TATAGCCTGG ACTTTCCTGT TGTCTACACC AATGCCCAAC TGCCTGCCTT |
| 151 | AGGCTAGTGC TAAGAGGATC TCCTGTCCAT CAGCCAGGAC AGTCAGCTCT |
| 201 | CTCCTTTCAG GGCCAATCCC CAGCCCTTTT GTTGAGCCAG GCCTCTCTCA |
| 251 | CCTCTCCTAC TCACTTAAAG CCCGCCCTGAC AGAACCACG GCCACATTTG |
| 301 | GTTCTAAGAA ACCCTCTGTC ATTGCTCCG ACATTCTGAT GAGCAACCGC |
| 351 | TTCCCTATTT <u>ATTATTTTAT</u> TTGTTTGTTT GTTTTATTCA TTGCTCTAAT |
| 401 | <u>TTATTCAAAG</u> GGGGCAAGAA GTAGCAGTGT CTGTAAGA GCCTAGTTTT |
| 451 | TAATAGCTAT GGAATCAATT CAATTGGAC TGGTGTGCTC TCTTAAATC |
| 501 | AAGTCCTTTA ATTAAGACTG AAAATATATA AGCTCAGATT <u>ATTAAATGG</u> |
| 551 | GAATATTTAT <u>AAATGAGCAA</u> ATATCACTACT GTTCAATGGT TCTGAATATA |
| 601 | ACTTCACCAT ATG |
| | NdeI |

Length: 613 bp

FIGURE 14

VEGF construct: 

■ AUUUA {Bold/Underline}

★ Potential polyA signal sequence {Bold/Italics}

Restriction Sites {Bold}

| | NotI | |
|------|--|------|
| 1 | GGGGCCGCAT TGCTGTGCTT TGGGGATTCC CTCCACATGC TGCACGCCA TCTCGCCCC AGGGGCACTG CCTGGAAGAT TCAGGAGCCT GGGCGGCCTT | |
| 101 | CGCTTACTCT CACCTGCTTC TGAGTGGCCC AGGAGGCCAC TGGCAGATGT CCCGGCGAAG AGAAGAGACA CATTGTTGGA AGAAGCAGCC CATGACAGCT | |
| 201 | CCCCCTCCTG GGACTCGCCC TCATCCTCTT CCTGCTCCCC TTCTTGGGT GCAGCCTAAA AGGACCTATG TCCTCACACC ATTGAAACCA CTAGTTCTGT | |
| 301 | CCCCCCAGGA GACCTGGTGT TGTGTGTGTG AGTGGTTGAC CTTCCTCCAT CCCCTGCTCC TTCCCGAGGC ACAGAGAGAC AGGGCAGGAT | |
| 401 | CCACGTGCCC ATTGTGGAGG CAGAGAAAAG AGAAGTGT TTATATACGG TACTTATTTA ATATCCCTTT TTAATTAGAA ATTAAAACAG TTAATTTAAT | |
| 501 | TAAAGAGTAG GGTTTTTTTT CAGTATTCTT GGTAAATATT TAATTTCAAC TATTTATGAG ATGTATCTTT TGCTCTCTCT TGCTCTCTTA TTTGTACCGG | |
| 601 | TTTTTGTATA TAAAAATCAT GTTCCAATC TCTCTCTCCC TGATCGGTGA CAGTCACTAG CTTATCTTGA ACAGATATTT AATTTTGCTA ACACTCAGCT | |
| 701 | CTGCCCTCCC CGATCCCCTG GCTCCCCCAGC ACACATTCCT TTGAATAAAG GTTCAATAT ACACTACAT ACTATATATA TATATTGGC AACTTGTATT | |
| 801 | TGTGTGTATA TATATATATA TATGTTTATG TATATATGT ATTCTGATAA AATAGACATT GCTATTCTGT TTTTATATG TAAAAACAAA ACAAGAAAAA | |
| 901 | ATAGAGAATT CTACATACTA AATCTCTCTC CTTTTTTTAA TTTAATATTT GTTATCATTT ATTATATGGT GCTACTGTTT ATCCGTAATA ATTGTGGGA | |
| 1001 | AAAGATATTA ACATCAGGTC TTTGTCTCTA GTGCAGTTTT TCGAGATATT CCGTAGTACA TATTTATTTT TAAACAACGA CAAAGAAATA CAGAACAATAT | |
| 1101 | G | NdeI |

Length: 1101 bp

FIGURE 15

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VEGF 3'UTR hypoxia domain construct:



■ AUUUA {Bold/Underline}
Restriction Sites {Bold}

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NotI
1  GCGGCCGCAT TCGTGTAGAC ACACCCACCC ACATACATAC ATTTATATAT
51 ATATATATTA TATATATATA AAAATAAATA TCTCTATTTT ATATATATAA
101 AATATATATA TTCTTTTTTT AAATTAACAG TGCTAATGTT ATTGGTGTCT
151 TCACTGGATG AACATATG
NdeI
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Length: 168 bp

FIGURE 16

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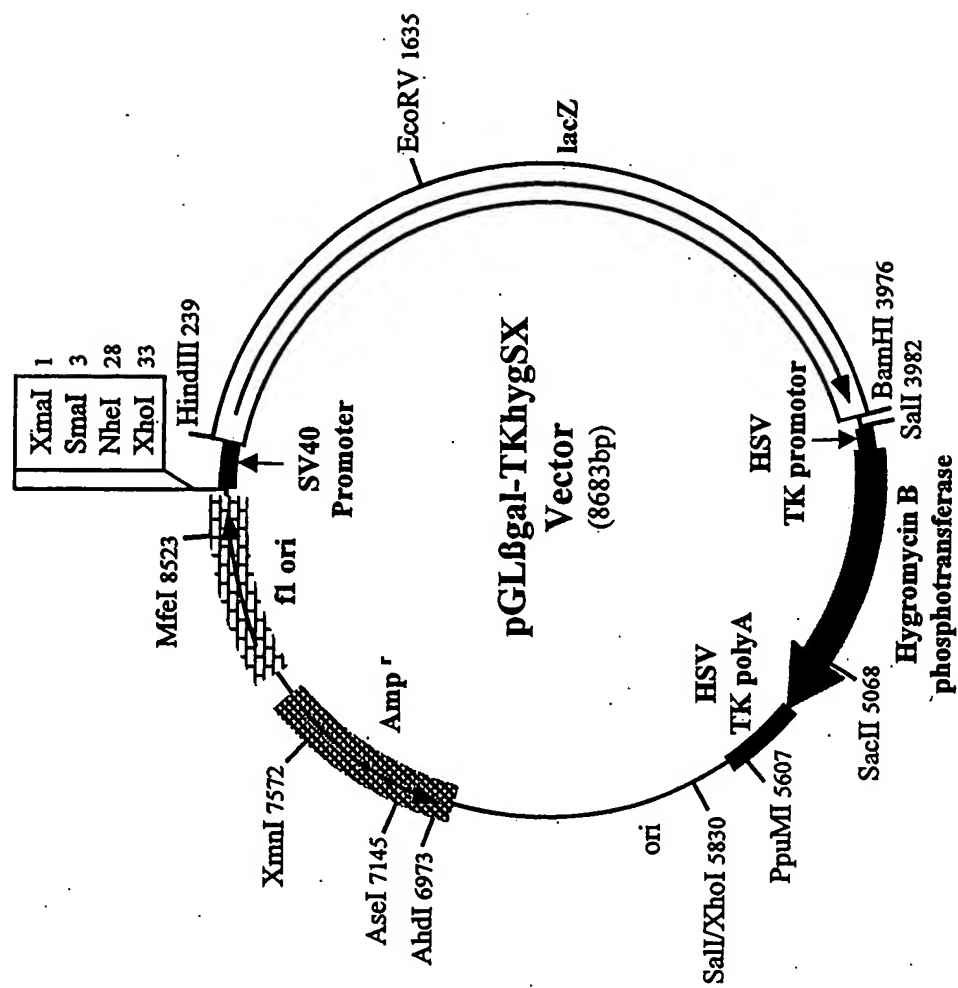


FIGURE 17